

Abstract

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A method for predicting the structure of a binding site to which a gene regulator binds, which method enables, through investigation of the internal structure of an enhancer or promoter, transcriptional regulation of a gene can be more clearly elucidated.

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The method for predicting the gene regulator binding site structure includes providing a gene of interest, of which a user of the method desires to predict regulation-related structures of binding sites (12), (13), (14) to which regulators bind, the binding sites (12), (13), (14) being present within an enhancer or promoter (11) region to which a protein serving as a transcriptional element is bound and which is present upstream or downstream to a coding region (15) of the gene; constructing a calculation model for each of the binding sites (12), (13), (14) within the enhancer or promoter (11) region, the binding sites (12), (13), (14) being such that relevant regulators or hypothetically introduced regulators are to be bound thereto, the calculation model employing, as parameters, loci of the regulator binding sites or other factors that cause expression of the gene; computing the level of transcription of the gene with respect to the above-constructed calculation model; searching, through use of parameter search algorithms, parameters of the calculation model so that empirically known expression of the gene is obtained; to thereby predict microstructures of the enhancer or promoter.